

Structural genomics of *Musa* using BAC sequences

Baurens Franc-Christophe

UMR DAP, CIRAD, Montpellier, France

Introduction

Banana cultivars are mostly highly sterile and parthenocarpic diploid or polyploid clones based only on the A genome from *Musa acuminata* or in combination with the B genome from *Musa balbisiana*. Several BAC libraries from wild and cultivated clones are available to study *Musa* genome structure. Through the Global Musa Genomic Consortium initiative with a Generation Challenge Program support, 50 banana BAC clones have been sequenced.

Musa Rice comparative genomics

To find out what degree of synteny (conservation of gene order) exists between the *Musa* and rice genomes, 17 BACs representing 1.8 Mb of sequence have been selected using gene markers conserved amongst Monocots (Lescot et al. 2008). Sequence analysis identified some micro-syntenic regions that have persisted over 117 Mya since the lineage of rice and *Musa* diverged. However, no general micro-syntenic conservation has been observed and numerous insertions and deletions of genes were found in between conserved sequence blocks. The *Musa* Rice comparative mapping strategy is then of limited efficiency for tagging genes.

Musa sp. Genomics

Based on two BAC pairs representing 104 kb of common sequence, a high level of synteny between *M. acuminata* (Genome A) and *M. balbisiana* (Genome B) has been found. This implies that the sequencing of one of these genomes will also benefit the other.

Musa haplotypes

Using MARGA08, a probe corresponding to a resistance gene analog (RGA) sequence, two BAC contigs from the wild species *M. balbisiana* have been identified and sequenced. Genetic mapping analyses, together with sequence comparison revealed that they corresponded to two haplotypes of a single locus. Genes and repetitive elements of the two contigs have been annotated revealing a cluster of a single family of cc-NBS-LRR type RGA. The sequences flanking the RGA cluster (80 kb) are highly conserved and only differ by SNP and SSR polymorphism, collinearity is however interrupted by the insertion of retroelements. The structure of the RGA cluster reveals some allelic relationships between RGA08 homologs but also numerous paralogs leading to a biased gene distribution between haplotypes. Phylogenetic analysis based on synonymous substitution rate on genic sequences together with LTR retroelements insertion datation allows for an estimation of haplotypes divergence within *M. balbisiana* of 1 My. Part of the BACs sequenced has also been selected using a collection of ethylene and cell wall biosynthesis related genes. Two paralogs of a Pectin methyl esterase gene (PME) have been discovered in a *M. acuminata* BAC. Expression pattern of these two genes are very different during ripening process of banana (M'Bégué et al. 2009). This

example emphasises how functional annotation in *Musa acuminata* BACs could support molecular physiology studies.

Conclusion

Sequencing BAC clone provided very useful informations on the *Musa* genome structure, on the relatedness between the A and B genomes that constitute the genomic pool of cultivated banana and also on the level of synteny with a sequenced model genome. These informations have been useful to set up the ANR project “MusaTract”. This project that aims at sequencing the genome of a double Haploid *Musa acuminata* accession is currently in progress.

References

- Lescot M, Piffanelli P, Ciampi AY, Ruiz M, Blanc G, Leebens-Mack J, da Silva FR, Santos CM, D'Hont A, Garsmeur O, Vilarinhos AD, Kanamori H, Matsumoto T, Ronning CM, Cheung F, Haas BJ, Althoff R, Arbogast T, Hine E, Pappas GJ, Jr., Sasaki T, Souza MT, Jr., Miller RN, Glaszmann JC, Town CD (2008) Insights into the Musa genome: syntenic relationships to rice and between Musa species. BMC Genomics 9:58. DOI 1471-2164-9-58
- Mbéguié-A-Mbéguié D., Hubert O., Baurens F.C., Matsumoto T., Chillet M., Fils-Lycaon B., Sidibé-Bocs S.(2009) Expression patterns of cell wall modifying genes from banana during fruit ripening and in relationship with finger drop. Journal of Experimental Botany Vol. 60, No. 7, pp. 2021–2034
- Franco-Christophe Baurens, Stephanie Sidibe-Bocs, Mathieu Rouard, Takashi Matsumoto, Robert Neil Gerard Miller, Marguerite Rodier-Goud, Didier M'Béguié a M'Béguié and, Nabila Yahiaoui Mechanisms of haplotype divergence at the RGA08 nucleotide-binding site leucine-rich repeat gene locus in wild banana (*Musa balbisiana*) In preparation